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(1) GENERAL INFORMATION:

- (i) APPLICANT: Gillespie, Alison
Claeps, Brian O.
Chavez-Noriega, Laura Elena
Siegel, Robert
Elliott, Kathryn J.
- (ii) TITLE OF INVENTION: DNA ENCODING HUMAN α AND β SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING
A HUMAN α AND β SUBUNITS OF NEURONAL
NICOTINIC ACETYLCHOLINE RECEPTOR
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Merck & Co., Inc.
(B) STREET: 126 E. Lincoln Avenue
(C) CITY: Rahway
(D) STATE: NJ
(E) COUNTRY: USA
(F) ZIP: 07065-0907
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/703,951
(B) FILING DATE: 01-NOV-2000
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/487,596
(B) FILING DATE: 07-JUN-1995
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO US94/02447
(B) FILING DATE: 08-MAR-1994
- (ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/149,503
(B) FILING DATE: 08-NOV-1993
- (x) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/028,031
(B) FILING DATE: 08-MAR-1993
- (xi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/938,154
(B) FILING DATE: 30-NOV-1992
- (xii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/504,455

(B) FILING DATE: 03-APR-1990

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kohli, Vineet
(B) REGISTRATION NUMBER: 37,003
(C) REFERENCE/DOCKET NUMBER: SD9951IA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 732-594-3889
(B) TELEFAX: 732-594-4720

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 166..1755
(D) OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGACCTG TTTTCTTCTG TAACCACAGG TTCGGTGGTG AGAGGAASCY TCGCAGAATC	60
CAGCAGAATC CTCACAGAAT CCAGCAGCAG CTCTGTGGG GACATGGTCC ATGGTGCAAC	120
CCACAGCAAA GCCCTGACCT GACCTCCTGA TGCTCAGGAG AAGCCATGGG CCCCTCCTGT	180
CCTGTGTTCC TGTCTTCAC AAAGCTCAGC CTGTGGTGGC TCCTTCTGAC CCCAGCAGGT	240
GGAGAGGAAG CTAAGCGCCC ACCTCCCAGG GCTCCTGGAG ACCCACTCTC CTCTCCCAGT	300
CCCACGGCAT TGCCGCAGGG AGGCTCGCAT ACCGAGACTG AGGACCGGCT CTTCAAACAC	360
CTCTTCCGGG GCTACAACCG CTGGGCGCGC CCGGTGCCCA AACTTCAGA CGTGGTGATT	420
GTGCGCTTTG GACTGTCCAT CGCTCAGCTC ATCGATGTGG ATGAGAAGAA CCAAATGATG	480
ACCACCAACG TCTGGCTAAA ACAGGAGTGG AGCGACTACA AACTGCGCTG GAACCCCGCT	540
GATTTTGGCA ACATCACATC TCTCAGGGTC CTTTCTGAGA TGATCTGGAT CCCCACATT	600
GTCTCTACA ACAATGCAGA TGGGGAGTTT GCAGTGACCC ACATGACCAA GGCCCACCTC	660
TTCTCCACGG GCACTGTGCA CTGGGTGCCC CCGGCCATCT ACAAGAGCTC CTGCAGCATC	720
GACGTCACCT TCTTCCCTT CGACCAGCAG AACTGCAAGA TGAAGTTTGG CTCCTGGACT	780
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TGGGAGAGCG GCGAGTGGG CATCGTCAAT GCCACGGGCA CCTACAACAG CAAGAAGTAC	900
GACTGCTGCG CCGAGATCTA CCCCACGTC ACCTACGCCT TCGTCATCCG GCGGCTGCCG	960

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CTCTTCTACA CCATCAACCT CATCATCCCC TGCCTGCTCA TCTCCTGCCT CACTGTGCTG 1020
GTCTTCTACC TGCCCTCCGA CTGCGGCGAG AAGATCACGC TGTGCATTTC GGTGCTGCTG 1080
TCACTCACCG TCTTCCTGCT GCTCATCACT GAGATCATCC CGTCCACCTC GCTGGTCATC 1140
CCGCTCATCG GCGAGTACCT GCTGTTTACC ATGATCTTCG TCACCCTGTC CATCGTCATC 1200
ACCGTCTTCG TGCTCAATGT GCACCACCGC TCCCCAGCA CCCACACCAT GCCCCACTGG 1260
GTGCGGGGGG CCCTTCTGGG CTGTGTGCCC CGGTGGCTTC TGATGAACCG GCCCCACCA 1320
CCCGTGGAGC TCTGCCACCC CCTACGCCTG AAGCTCAGCC CCTCTTATCA CTGGCTGGAG 1380
AGCAACGTGG ATGCCGAGGA GAGGGAGGTG GTGGTGGAGG AGGAGGACAG ATGGGCATGT 1440
GCAGGTCATG TGGCCCCCTC TGTGGGCACC CTCTGCAGCC ACGGCCACCT GCACTCTGGG 1500
GCCTCAGGTC CCAAGGCTGA GGCTCTGCTG CAGGAGGGTG AGCTGCTGCT ATCACCCAC 1560
ATGCAGAAGG CACTGGAAGG TGTGCACTAC ATTGCCGACC ACCTGCGGTC TGAGGATGCT 1620
GACTCTTCGG TGAAGGAGGA CTGGAAGTAT GTTGCCATGG TCATCGACAG GATCTTCCTC 1680
TGGCTGTTTA TCATCGTCTG CTTCTGCGG ACCATCGGCC TCTTTCTGCC TCCGTTCCCTA 1740
GCTGGAATGA TCTGACTGCA CCTCCCTCGA GCTGGCTCCC AGGGCAAAGG GGAGGGTTCT 1800
TGGATGTGGA AGGGCTTTGA ACAATGTTTA GATTGTGAGA TGAGCCCAAA GTGCCAGGGA 1860
GAACAGCCAG GTGAGGTGGG AGGTGTGAGA GCCAGGTGAG GTCTCTCTAA GTCAGGCTGG 1920
GGTTGAAGTT TGGAGTCTGT CCGAGTTTGC AGGGTGCTGA GCTGTATGGT CCAGCAGGGG 1980
AGTAATAAGG GCTCTTCCGG AAGGGGAGGA AGCGGGAGGC AGGGCCTGCA CCTGATGTGG 2040
AGGTACAGGG CAGATCTTCC CTACCGGGGA GGGATGGATG GTTGGATACA GGTGGCTGGG 2100
CTATTCCATC CATCTGGAAG CACATTGAG CCTCCAGGCT TCTCCTTGAC GTCATTCTC 2160
TCCTTCCTTG CTCCAAAATG GCTCTGCACC AGCCGGCCCC CAGGAGGTCT GGCAGAGCTG 2220
AGAGCCATGG CCTGCAGGGG CTCCATATGT CCCTACGCGT GCAGCAGGCA AACAAGA 2277

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Pro Ser Cys Pro Val Phe Leu Ser Phe Thr Lys Leu Ser Leu
1           5           10           15

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Trp Trp Leu Leu Leu Thr Pro Ala Gly Gly Glu Glu Ala Lys Arg Pro

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20					25					30					
Pro	Pro	Arg	Ala	Pro	Gly	Asp	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Thr	Ala
		35					40					45			
Leu	Pro	Gln	Gly	Gly	Ser	His	Thr	Glu	Thr	Glu	Asp	Arg	Leu	Phe	Lys
	50					55					60				
His	Leu	Phe	Arg	Gly	Tyr	Asn	Arg	Trp	Ala	Arg	Pro	Val	Pro	Asn	Thr
	65					70					75				80
Ser	Asp	Val	Val	Ile	Val	Arg	Phe	Gly	Leu	Ser	Ile	Ala	Gln	Leu	Ile
				85					90					95	
Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr	Asn	Val	Trp	Leu	Lys
			100					105					110		
Gln	Glu	Trp	Ser	Asp	Tyr	Lys	Leu	Arg	Trp	Asn	Pro	Ala	Asp	Phe	Gly
		115					120					125			
Asn	Ile	Thr	Ser	Leu	Arg	Val	Pro	Ser	Glu	Met	Ile	Trp	Ile	Pro	Asp
	130					135					140				
Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Glu	Phe	Ala	Val	Thr	His	Met
	145					150					155				160
Thr	Lys	Ala	His	Leu	Phe	Ser	Thr	Gly	Thr	Val	His	Trp	Val	Pro	Pro
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Ala	Ile	Tyr	Lys	Ser	Ser	Cys	Ser	Ile	Asp	Val	Thr	Phe	Phe	Pro	Phe
			180					185					190		
Asp	Gln	Gln	Asn	Cys	Lys	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Lys
		195					200					205			
Ala	Lys	Ile	Asp	Leu	Glu	Gln	Met	Glu	Gln	Thr	Val	Asp	Leu	Lys	Asp
	210					215					220				
Tyr	Trp	Glu	Ser	Gly	Glu	Trp	Ala	Ile	Val	Asn	Ala	Thr	Gly	Thr	Tyr
	225					230					235				240
Asn	Ser	Lys	Lys	Tyr	Asp	Cys	Cys	Ala	Glu	Ile	Tyr	Pro	Asp	Val	Thr
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Tyr	Ala	Phe	Val	Ile	Arg	Arg	Leu	Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu
			260					265					270		
Ile	Ile	Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	Val	Leu	Val	Phe	Tyr
		275					280					285			
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	290					295					300				
Leu	Ser	Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	Glu	Ile	Ile	Pro	Ser
	305					310					315				320
Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Thr	Met
			325						330					335	
Ile	Phe	Val	Thr	Leu	Ser	Ile	Val	Ile	Thr	Val	Phe	Val	Leu	Asn	Val
			340					345					350		

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His His Arg Ser Pro Ser Thr His Thr Met Pro His Trp Val Arg Gly
   355                                360                                365

Ala Leu Leu Gly Cys Val Pro Arg Trp Leu Leu Met Asn Arg Pro Pro
   370                                375                                380

Pro Pro Val Glu Leu Cys His Pro Leu Arg Leu Lys Leu Ser Pro Ser
  385                                390                                395                                400

Tyr His Trp Leu Glu Ser Asn Val Asp Ala Glu Glu Arg Glu Val Val
      405                                410                                415

Val Glu Glu Glu Asp Arg Trp Ala Cys Ala Gly His Val Ala Pro Ser
      420                                425                                430

Val Gly Thr Leu Cys Ser His Gly His Leu His Ser Gly Ala Ser Gly
      435                                440                                445

Pro Lys Ala Glu Ala Leu Leu Gln Glu Gly Glu Leu Leu Leu Ser Pro
      450                                455                                460

His Met Gln Lys Ala Leu Glu Gly Val His Tyr Ile Ala Asp His Leu
  465                                470                                475                                480

Arg Ser Glu Asp Ala Asp Ser Ser Val Lys Glu Asp Trp Lys Tyr Val
      485                                490                                495

Ala Met Val Ile Asp Arg Ile Phe Leu Trp Leu Phe Ile Ile Val Cys
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Phe Leu Gly Thr Ile Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met
      515                                520                                525

Ile

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 39..1553
- (D) OTHER INFORMATION: /product= "ALPHA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCAGGGCCTC AGAGGCTGAG CACCGTCTAT TTGAGCGGCT GTTTGAAGAT TACAATGAGA      180

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TCATCCGGCC TGTAGCCAAC GTGTCTGACC CAGTCATCAT CCATTTCGAG GTGTCCATGT	240
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AAATCTGGAA TGACTACAAG CTGAAGTGA ACCCCTCTGA CTATGGTGGG GCAGAGTTCA	360
TGCGTGTCCC TGCACAGAAG ATCTGGAAGC CAGACATTGT GCTGTATAAC AATGCTGTTG	420
GGGATTTCCA GGTGGACGAC AAGACCAAAG CCTTACTCAA GTACACTGGG GAGGTGACTT	480
GGATACCTCC GGCCATCTTT AAGAGCTCCT GTAAAATCGA CGTGACCTAC TTCCCGTTTG	540
ATTACCAAAA CTGTACCATG AAGTTCGGTT CCTGGTCCTA CGATAAGGCG AAAATCGATC	600
TGGTCCTGAT CGGCTCTTCC ATGAACCTCA AGGACTATTG GGAGAGCGGC GAGTGGGCCA	660
TCATCAAAGC CCCAGGCTAC AAACACGACA TCAAGTACAG CTGCTGCGAG GAGATCTACC	720
CCGACATCAC ATACTCGCTG WWCATCCGGC GGCTGTCGTT GTTCTACACC ATCAWCCTCA	780
TCATCCGCTG GCTGATCATC TCCTTCATCA CTGTGGTCGT CTCTACCTG CCCTCCGACT	840
GCGGCGAGAA GGTGACCCCTG TGYATTTCTG TCCTCCTCTC CCTGACGGTG TTTCTCCTGG	900
TGATCACTGA GACCATCCCT TCCACCTCGC TGGTCATCCC CCTGATTGGA GAGTACCTCC	960
TGWWACCAT GATTTGTGTA ACCTTGTCCTA TCGACATCAC CGTCTGCGTG CTCAACGTGC	1020
ACTACAGAAC CCCGACGACA CACACAATGC CCTCATGGGT GAAGACTGTA TTCTTGAMCC	1080
TGCTCCCCAG GGTCATGTWC ATGACCAGGC CAACAAGCAA CGAGGGCAAC GCTCAGAAGC	1140
CGAGGCCCCCT CTACGGTGCC GAGCTCTCAA ATCTGAATTG CTTAGCCGC GCAGAGTCCA	1200
AAGGCTGCAA GGAGGGCTAC CCCTGCCAGG ACGGGATGTG TGGTTACTGC CACCACCGCA	1260
GGATAAAAAT CTCCAATTTT AGTGCTAACC TCACGAGAAG CTCTAGTTCT GAATCTGTTG	1320
ATGCTGTGCT GTCCCTCTCT GCTTTGTCAC CAGAAATCAA AGAAGCCATC CAAAGTGTC	1380
AGTATATTGC TGAAAATATG AAAGCACAAA ATGAAGCCAA AGAGATTCAA GATGATTGGA	1440
AGTATGTTGC CATGGTGATT GATCGTATTT TTCTGTGGGT TTTACCCCTG GTGTGCATTC	1500
TAGGGACAGC AGGATTGTTT CTGCAACCCC TGATGGCCAG GGAAGATGCA TAAGCACTAA	1560
GCTGTGTGCC TGCCTGGGAG ACTTCCTTGT GTCAGGGCAG GAGGAGGCTG CTTCTAGTA	1620
AGAACGTA CTCTGTTATC AAGCTACCAG CTTT	1654

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ser Gly Pro Leu Ser Leu Pro Leu Ala Leu Ser Pro Pro Arg
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 Ala Glu His Arg Leu Phe Glu Arg Leu Phe Glu Asp Tyr Asn Glu Ile
 35 40 45
 Ile Arg Pro Val Ala Asn Val Ser Asp Pro Val Ile Ile His Phe Glu
 50 55 60
 Val Ser Met Ser Gln Leu Val Lys Val Asp Glu Val Asn Gln Ile Met
 65 70 75 80
 Glu Thr Asn Leu Trp Leu Lys Gln Ile Trp Asn Asp Tyr Lys Leu Lys
 85 90 95
 Trp Asn Pro Ser Asp Tyr Gly Gly Ala Glu Phe Met Arg Val Pro Ala
 100 105 110
 Gln Lys Ile Trp Lys Pro Asp Ile Val Leu Tyr Asn Asn Ala Val Gly
 115 120 125
 Asp Phe Gln Val Asp Asp Lys Thr Lys Ala Leu Leu Lys Tyr Thr Gly
 130 135 140
 Glu Val Thr Trp Ile Pro Pro Ala Ile Phe Lys Ser Ser Cys Lys Ile
 145 150 155 160
 Asp Val Thr Tyr Phe Pro Phe Asp Tyr Gln Asn Cys Thr Met Lys Phe
 165 170 175
 Gly Ser Trp Ser Tyr Asp Lys Ala Lys Ile Asp Leu Val Leu Ile Gly
 180 185 190
 Ser Ser Met Asn Leu Lys Asp Tyr Trp Glu Ser Gly Glu Trp Ala Ile
 195 200 205
 Ile Lys Ala Pro Gly Tyr Lys His Asp Ile Lys Tyr Ser Cys Cys Glu
 210 215 220
 Glu Ile Tyr Pro Asp Ile Thr Tyr Ser Leu Xaa Ile Arg Arg Leu Ser
 225 230 235 240
 Leu Phe Tyr Thr Ile Xaa Leu Ile Ile Arg Trp Leu Ile Ile Ser Phe
 245 250 255
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 260 265 270
 Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Val
 275 280 285
 Ile Thr Glu Thr Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly
 290 295 300
 Glu Tyr Leu Leu Xaa Thr Met Ile Cys Val Thr Leu Ser Ile Asp Ile
 305 310 315 320
 Thr Val Cys Val Leu Asn Val His Tyr Arg Thr Pro Thr Thr His Thr

				325					330					335		
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Met	Xaa	Met 355	Thr	Arg	Pro	Thr	Ser 360	Asn	Glu	Gly	Asn	Ala 365	Gln	Lys	Pro	
Arg	Pro 370	Leu	Tyr	Gly	Ala	Glu 375	Leu	Ser	Asn	Leu	Asn 380	Cys	Phe	Ser	Arg	
Ala 385	Glu	Ser	Lys	Gly	Cys 390	Lys	Glu	Gly	Tyr	Pro 395	Cys	Gln	Asp	Gly	Met 400	
Cys	Gly	Tyr	Cys	His 405	His	Arg	Arg	Ile	Lys 410	Ile	Ser	Asn	Phe	Ser	Ala 415	
Asn	Leu	Thr	Arg 420	Ser	Ser	Ser	Ser	Glu 425	Ser	Val	Asp	Ala	Val 430	Leu	Ser	
Leu	Ser	Ala 435	Leu	Ser	Pro	Glu	Ile 440	Lys	Glu	Ala	Ile	Gln 445	Ser	Val	Lys	
Tyr	Ile 450	Ala	Glu	Asn	Met	Lys 455	Ala	Gln	Asn	Glu	Ala 460	Lys	Glu	Ile	Gln	
Asp 465	Asp	Trp	Lys	Tyr	Val 470	Ala	Met	Val	Ile	Asp 475	Arg	Ile	Phe	Leu	Trp 480	
Val	Phe	Thr	Leu	Val 485	Cys	Ile	Leu	Gly	Thr 490	Ala	Gly	Leu	Phe	Leu 495	Gln	
Pro	Leu	Met	Ala 500	Arg	Glu	Asp	Ala									

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 173..2056
(D) OTHER INFORMATION: /product= "ALPHA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CGGCCGAAGC	GGCCCGCGAG	GCGCGGGAGG	CATGAAGTTG	GCGCGCACG	GGCCTCGAAG	120
CGGCGGGGAG	CCGGGAGCCG	CCCGCATCTA	GAGCCC GCGA	GGTGCGTGCG	CCATGGAGCT	180
AGGGGGCCCC	GGAGCGCCGC	GGCTGCTGCC	GCCGCTGCTG	CTGCTTCTGG	GGACCGGCCT	240

CCTGCGCGCC AGCAGCCATG TGGAGACCCG GGCCACGCC GAGGAGCGGC TCCTGAAGAA	300
ACTCTTCTCC GGTTACAACA AGTGGTCCCG ACCCGTGGCC AACATCTCGG ACGTGGTCCT	360
CGTCCGCTTC GGCTGTCCA TCGCTCAGCT CATTGACGTG GATGAGAAGA ACCAGATGAT	420
GACCACGAAC GTCTGGGTGA AGCAGGAGTG GCACGACTAC AAGCTGCGCT GGGACCCAGC	480
TGACTATGAG AATGTCACCT CCATCCGCAT CCCCTCCGAG CTCATCTGGC GGCCGGACAT	540
CGCCCTCTAC AACAATGCTG ACGGGGACTT CGCGGCCACC CACCTGACCA AGGCCACCT	600
GTTCATGAC GGGCGGGTGC AGCGGACTCC CCCGGCCATT TACAAGAGCT CCTGCAGCAT	660
CGACGTCACC TTCTTCCCT TCGACCAGCA GAAGTGCACC ATGAAATTCG GCTCCTGGAC	720
CTACGACAAG GCCAAGATCG ACCTGGTGAA CATGCACAGC CGCGTGGACC AGCTGGACTT	780
CTGGGAGAGT GGCAGAGTGGC TCATCTCGGA CGCCGTGGGC ACCTACAACA CCAGGAAGTA	840
CGAGTGCTGC GCCGAGATCT ACCCGGACAT CACCTATGCC TACGCCATCC GGCGGGTGCC	900
GCTCTTCTAC ACCATCAACC TCATCATCCC CTGGCTGCTC ATCTCCTGCC TCACCGCGCT	960
GGTCTTCTAC CTGCCCTCCG AGTGTGGCGA GAAGATCAGC CTGTGCATCT CCGTGTGCT	1020
GTCGCTCACC GTCTTCCTGC TGCTCATCAC CGAGATCATC CCGTCCACCT CACTGGTCAT	1080
CCCACTCATC GGCAGTACC TGCTGTTTAC CATGATCTTC GTCACCCTGT CCATCGCCAT	1140
CACGGTCTTC GTGCTCAACG TGCACCACCG CTCGCCACGC ACGCACACCA TGCCCACCTG	1200
GGTACGAGG GTCTTCCTGG ACATCGTGCC ACGCTGCTC CTCATGAAGC GGCCGTCCGT	1260
GGTCAAGGAC AATTGCCGGC GGCTCATCGA GTCCATGCAT AAGATGGCCA GTGCCCCGCG	1320
CTTCTGGCCC GAGCCAGAAG GGGAGCCCC TGCCACGAGC GGCACCCAGA GCCTGCACCC	1380
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CCCCTCGCCT GGACCCTGCC GCGCGCCCA CGGCACCCAG GCACCAGGGC TGGCCAAAGC	1560
CAGGTCCCTC AGCGTCCAGC ACATGTCCAG CCCTGGCGAA GCGGTGGAAG GCGGCGTCCG	1620
GTGCCGGTCT CGGAGCATCC AGTACTGTGT TCCCCGAGAC GATGCCGCC CCGAGGCAGA	1680
TGGCCAGGCT GCCGGCGCCC TGGCTCTCG CAACAGCCAC TCGGCTGAGC TCCCACCCCC	1740
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CGCCACGGTC AAGACCCGCA GCACCAAAGC GCCGCCGCC CACCTGCCCC TGTCGCCGGC	1860
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CTGGATGTTT ATCATCGTCT GCCTGCTGGG GACGGTGGGC CTCTTCCTGC CGCCCTGGCT	2040
GGCTGGCATG ATCTAGGAAG GGACCGGGAG CCTGCGTGGC CTGGGGCTGC CGYGCACGGG	2100

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GCCAGCATCC ATGCGGCCGG CCTGGGGCCG GGCTGGCTTC TCCCTGGACT CTGTGGGGCC 2160
ACACGTTTGC CAAATTTTCC TTCCTGTTCT GTGTCTGCTG TAAGACGGCC TTGGACGGCG 2220
ACACGGCCTC TGGGGAGACC GAGTGTGGAG CTGCTTCCAG TTGGACTCTS GCCTCAGNAG 2280
GCAGCGGCTT GGAGCAGAGG TGGCGGTCGC CGCCTYCTAC CTGCAGGACT CGGGCTAAGT 2340
CCAGCTCTCC CCCTGCGCAG CCC 2363

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 627 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Glu Leu Gly Gly Pro Gly Ala Pro Arg Leu Leu Pro Pro Leu Leu
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20     25     30
Arg Ala His Ala Glu Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr
35     40     45
Asn Lys Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val Leu Val
50     55     60
Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn
65     70     75     80
Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr
85     90     95
Lys Leu Arg Trp Asp Pro Ala Asp Tyr Glu Asn Val Thr Ser Ile Arg
100    105    110
Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Ala Leu Tyr Asn Asn
115    120    125
Ala Asp Gly Asp Phe Ala Ala Thr His Leu Thr Lys Ala His Leu Phe
130    135    140
His Asp Gly Arg Val Gln Arg Thr Pro Pro Ala Ile Tyr Lys Ser Ser
145    150    155    160
Cys Ser Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr
165    170    175
Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val
180    185    190
Asn Met His Ser Arg Val Asp Gln Leu Asp Phe Trp Glu Ser Gly Glu
195    200    205

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Trp Leu Ile Ser Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu
 210 215 220
 Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Tyr Ala Ile Arg
 225 230 235 240
 Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Trp Leu Leu
 245 250 255
 Ile Ser Cys Leu Thr Ala Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly
 260 265 270
 Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe
 275 280 285
 Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro
 290 295 300
 Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser
 305 310 315 320
 Ile Ala Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg
 325 330 335
 Thr His Thr Met Pro Thr Trp Val Arg Arg Val Phe Leu Asp Ile Val
 340 345 350
 Pro Arg Leu Leu Leu Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys
 355 360 365
 Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Ser Ala Pro Arg Phe
 370 375 380
 Trp Pro Glu Pro Glu Gly Glu Pro Pro Ala Thr Ser Gly Thr Gln Ser
 385 390 395 400
 Leu His Pro Pro Ser Pro Ser Phe Cys Val Pro Leu Asp Val Pro Ala
 405 410 415
 Glu Pro Gly Pro Ser Cys Lys Ser Pro Ser Asp Gln Leu Pro Pro Gln
 420 425 430
 Gln Pro Leu Glu Ala Glu Lys Ala Ser Pro His Pro Ser Pro Gly Pro
 435 440 445
 Cys Arg Pro Pro His Gly Thr Gln Ala Pro Gly Leu Ala Lys Ala Arg
 450 455 460
 Ser Leu Ser Val Gln His Met Ser Ser Pro Gly Glu Ala Val Glu Gly
 465 470 475 480
 Gly Val Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Pro Arg Asp
 485 490 495
 Asp Ala Ala Pro Glu Ala Asp Gly Gln Ala Ala Gly Ala Leu Ala Ser
 500 505 510
 Arg Asn Ser His Ser Ala Glu Leu Pro Pro Pro Asp Gln Pro Ser Pro
 515 520 525
 Cys Lys Cys Thr Cys Lys Lys Glu Pro Ser Ser Val Ser Pro Ser Ala

530	535	540
Thr Val Lys Thr Arg Ser Thr Lys Ala Pro Pro Pro His Leu Pro Leu		
545	550	555
Ser Pro Ala Leu Ser Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp		
	565	570
		575
His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys		
	580	585
		590
Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile		
	595	600
		605
Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala		
	610	615
		620
Gly Met Ile		
625		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 155..1561
- (D) OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCCGCGGGA GCTGTGGCGC GGAGCGGCCC CGCTGCTGCG TCTGCCCTCG TTTTGTCTCA	60
CGACTCACAC TCAGTGCTGC ATTCCTCAAG AGTTCGCGTT CCCC GCGCGG CGGTCGAGAG	120
GCGGCTGCCC GCGGTCCCGC GCGGGCGCGG GGCG ATG GCG GCG CGG GGG TCA	172
Met Ala Ala Arg Gly Ser	
1 5	
GGG CCC CGC GCG CTC CGC CTG CTG CTC TTG GTC CAG CTG GTC GCG GGG	220
Gly Pro Arg Ala Leu Arg Leu Leu Leu Val Gln Leu Val Ala Gly	
10 15 20	
CGC TGC GGT CTA GCG GGC GCG GCG GGC GCG CAG AGA GGA TTA TCT	268
Arg Cys Gly Leu Ala Gly Ala Ala Gly Gly Ala Gln Arg Gly Leu Ser	
25 30 35	
GAA CCT TCT TCT ATT GCA AAA CAT GAA GAT AGT TTG CTT AAG GAT TTA	316
Glu Pro Ser Ser Ile Ala Lys His Glu Asp Ser Leu Leu Lys Asp Leu	
40 45 50	
TTT CAA GAC TAC GAA AGA TGG GTT CGT CCT GTG GAA CAC CTG AAT GAC	364
Phe Gln Asp Tyr Glu Arg Trp Val Arg Pro Val Glu His Leu Asn Asp	

55	60	65	70	
AAA ATA AAA ATA AAA TTT GGA CTT GCA ATA TCT CAA TTG GTG GAT GTG Lys Ile Lys Ile Lys Phe Gly Leu Ala Ile Ser Gln Leu Val Asp Val 75 80 85				412
GAT GAG AAA AAT CAG TTA ATG ACA ACA AAC GTC TGG TTG AAA CAG GAA Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu 90 95 100				460
TGG ATA GAT GTA AAA TTA AGA TGG AAC CCT GAT GAC TAT GGT GGA ATA Trp Ile Asp Val Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile 105 110 115				508
AAA GTT ATA CGT GTT CCT TCA GAC TCT GTC TGG ACA CCA GAC ATC GTT Lys Val Ile Arg Val Pro Ser Asp Ser Val Trp Thr Pro Asp Ile Val 120 125 130				556
TTG TTT GAT AAT GCA GAT GGA CGT TTT GAA GGG ACC AGT ACG AAA ACA Leu Phe Asp Asn Ala Asp Gly Arg Phe Glu Gly Thr Ser Thr Lys Thr 135 140 145 150				604
GTC ATC AGG TAC AAT GGC ACT GTC ACC TGG ACT CCA CCG GCA AAC TAC Val Ile Arg Tyr Asn Gly Thr Val Thr Trp Thr Pro Pro Ala Asn Tyr 155 160 165				652
AAA AGT TCC TGT ACC ATA GAT GTC ACG TTT TTC CCA TTT GAC CTT CAG Lys Ser Ser Cys Thr Ile Asp Val Thr Phe Phe Pro Phe Asp Leu Gln 170 175 180				700
AAC TGT TCC ATG AAA TTT GGT TCT TGG ACT TAT GAT GGA TCA CAG GTT Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Ser Gln Val 185 190 195				748
GAT ATA ATT CTA GAG GAC CAA GAT GTA GAC AAG AGA GAT TTT TTT GAT Asp Ile Ile Leu Glu Asp Gln Asp Val Asp Lys Arg Asp Phe Phe Asp 200 205 210				796
AAT GGA GAA TGG GAG ATT GTG AGT GCA ACA GGG AGC AAA GGA AAC AGA Asn Gly Glu Trp Glu Ile Val Ser Ala Thr Gly Ser Lys Gly Asn Arg 215 220 225 230				844
ACC GAC AGC TGT TGC TGG TAT CCG TAT GTC ACT TAC TCA TTT GTA ATC Thr Asp Ser Cys Cys Trp Tyr Pro Tyr Val Thr Tyr Ser Phe Val Ile 235 240 245				892
AAG CGC CTG CCT CTC TTT TAT ACC TTG TTC CTT ATA ATA CCC TGT ATT Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Ile 250 255 260				940
GGG CTC TCA TTT TTA ACT GTA CTT GTC TTC TAT CTT CCT TCA AAT GAA Gly Leu Ser Phe Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Asn Glu 265 270 275				988
GGT GAA AAG ATT TGT CTC TGC ACT TCA GTA CTT GTG TCT TTG ACT GTC Gly Glu Lys Ile Cys Leu Cys Thr Ser Val Leu Val Ser Leu Thr Val 280 285 290				1036
TTC CTT CTG GTT ATT GAA GAG ATC ATA CCA TCA TCT TCA AAA GTC ATA Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser Ser Ser Lys Val Ile 295 300 305 310				1084

CCT CTA ATT GGA GAG TAT CTG GTA TTT ACC ATG ATT TTT GTG ACA CTG	1132
Pro Leu Ile Gly Glu Tyr Leu Val Phe Thr Met Ile Phe Val Thr Leu	
315 320 325	
TCA ATT ATG GTA ACC GTC TTC GCT ATC AAC ATT CAT CAT CGT TCT TCC	1180
Ser Ile Met Val Thr Val Phe Ala Ile Asn Ile His His Arg Ser Ser	
330 335 340	
TCA ACA CAT AAT GCC ATG GCG CCT TTG GTC CGC AAG ATA TTT CTT CAC	1228
Ser Thr His Asn Ala Met Ala Pro Leu Val Arg Lys Ile Phe Leu His	
345 350 355	
ACG CTT CCC AAA CTG CTT TGC ATG AGA AGT CAT GTA GAC AGG TAC TTC	1276
Thr Leu Pro Lys Leu Leu Cys Met Arg Ser His Val Asp Arg Tyr Phe	
360 365 370	
ACT CAG AAA GAG GAA ACT GAG AGT GGT AGT GGA CCA AAA TCT TCT AGA	1324
Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro Lys Ser Ser Arg	
375 380 385 390	
AAC ACA TTG GAA GCT GCG CTC AAT TCT ATT CGC TAC ATT ACA AGA CAC	1372
Asn Thr Leu Glu Ala Ala Leu Asn Ser Ile Arg Tyr Ile Thr Arg His	
395 400 405	
ATC ATG AAG GAA AAT GAT GTC CGT GAG GTT GTT GAA GAT TGG AAA TTC	1420
Ile Met Lys Glu Asn Asp Val Arg Glu Val Val Glu Asp Trp Lys Phe	
410 415 420	
ATA GCC CAG GTT CTT GAT CGG ATG TTT CTG TGG ACT TTT CTT TTC GTT	1468
Ile Ala Gln Val Leu Asp Arg Met Phe Leu Trp Thr Phe Leu Phe Val	
425 430 435	
TCA ATT GTT GGA TCT CTT GGG CTT TTT GTT CCT GTT ATT TAT AAA TGG	1516
Ser Ile Val Gly Ser Leu Gly Leu Phe Val Pro Val Ile Tyr Lys Trp	
440 445 450	
GCA AAT ATA TTA ATA CCA GTT CAT ATT GGA AAT GCA AAT AAG TGAAGCCTCC	1568
Ala Asn Ile Leu Ile Pro Val His Ile Gly Asn Ala Asn Lys	
455 460 465	
CAAGGGACTG AAGTATACAT TTAGTTAACA CACATATATC TGATGGCACC TATAAAATTA	1628
TGAAAATGTA AGTTATGTGT TAAATTTAGT GCAAGCTTTA ACAGACTAAG TTGCTAACCT	1688
CAATTTATGT TAACAGATGA TCCATTTGAA CAGTTGGCTG TATGACTGAA GTAATAACTG	1748
ATGAGATACA TTTGATCTTG TAAAAATAGC AAAATATTAT CTGAACTGGA CTAGTGAAAA	1808
ATCTAGTATT TGTATCCTGG	1828

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	325		330		335
Ile His His Arg Ser Ser Ser Thr His Asn Ala Met Ala Pro Leu Val	340		345		350
Arg Lys Ile Phe Leu His Thr Leu Pro Lys Leu Leu Cys Met Arg Ser	355		360		365
His Val Asp Arg Tyr Phe Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser	370		375		380
Gly Pro Lys Ser Ser Arg Asn Thr Leu Glu Ala Ala Leu Asn Ser Ile	385		390		395
Arg Tyr Ile Thr Arg His Ile Met Lys Glu Asn Asp Val Arg Glu Val	405		410		415
Val Glu Asp Trp Lys Phe Ile Ala Gln Val Leu Asp Arg Met Phe Leu	420		425		430
Trp Thr Phe Leu Phe Val Ser Ile Val Gly Ser Leu Gly Leu Phe Val	435		440		445
Pro Val Ile Tyr Lys Trp Ala Asn Ile Leu Ile Pro Val His Ile Gly	450		455		460
Asn Ala Asn Lys	465				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 143..1627
- (D) OTHER INFORMATION: /product= "ALPHA-6 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGTTTTGA TTTCTGAGAA GACACACACG GATTGCAGTG GGCTTCTGAT GATGTCAAGG	60
TTGGATGCAT GTGGCTGACT GATAGCTCTT TGTTTTCCAC AATCCTTTGC CTAGGAAAAA	120
GGAATCCAAG TGTGTTTTAA CC ATG CTG ACC AGC AAG GGG CAG GGA TTC CTT	172
Met Leu Thr Ser Lys Gly Gln Gly Phe Leu	10
CAT GGG GGC TTG TGT CTC TGG CTG TGT GTG TTC ACA CCT TTC TTT AAA	220
His Gly Gly Leu Cys Leu Trp Leu Cys Val Phe Thr Pro Phe Phe Lys	25
GGC TGT GTG GGC TGT GCA ACT GAG GAG AGG CTC TTC CAC AAA CTG TTT	268

Gly	Cys	Val	Gly	Cys	Ala	Thr	Glu	Glu	Arg	Leu	Phe	His	Lys	Leu	Phe		
			30					35					40				
TCT	CAT	TAC	AAC	CAG	TTC	ATC	AGG	CCT	GTG	GAA	AAC	GTT	TCC	GAC	CCT	316	
Ser	His	Tyr	Asn	Gln	Phe	Ile	Arg	Pro	Val	Glu	Asn	Val	Ser	Asp	Pro		
		45					50					55					
GTC	ACG	GTA	CAC	TTT	GAA	GTG	GCC	ATC	ACC	CAG	CTG	GCC	AAC	GTG	GAT	364	
Val	Thr	Val	His	Phe	Glu	Val	Ala	Ile	Thr	Gln	Leu	Ala	Asn	Val	Asp		
	60					65					70						
GAA	GTA	AAC	CAG	ATC	ATG	GAA	ACC	AAT	TTG	TGG	CTG	CGT	CAC	ATC	TGG	412	
Glu	Val	Asn	Gln	Ile	Met	Glu	Thr	Asn	Leu	Trp	Leu	Arg	His	Ile	Trp		
	75				80					85					90		
AAT	GAT	TAT	AAA	TTG	CGC	TGG	GAT	CCA	ATG	GAA	TAT	GAT	GGC	ATT	GAG	460	
Asn	Asp	Tyr	Lys	Leu	Arg	Trp	Asp	Pro	Met	Glu	Tyr	Asp	Gly	Ile	Glu		
			95					100						105			
ACT	CTT	CGC	GTT	CCT	GCA	GAT	AAG	ATT	TGG	AAG	CCC	GAC	ATT	GTT	CTC	508	
Thr	Leu	Arg	Val	Pro	Ala	Asp	Lys	Ile	Trp	Lys	Pro	Asp	Ile	Val	Leu		
			110					115					120				
TAT	AAC	AAT	GCT	GTT	GGT	GAC	TTC	CAA	GTA	GAA	GGC	AAA	ACA	AAA	GCT	556	
Tyr	Asn	Asn	Ala	Val	Gly	Asp	Phe	Gln	Val	Glu	Gly	Lys	Thr	Lys	Ala		
			125				130					135					
CTT	CTT	AAA	TAC	AAT	GGC	ATG	ATA	ACC	TGG	ACT	CCA	CCA	GCT	ATT	TTT	604	
Leu	Leu	Lys	Tyr	Asn	Gly	Met	Ile	Thr	Trp	Thr	Pro	Pro	Ala	Ile	Phe		
			140			145					150						
AAG	AGT	TCC	TGC	CCT	ATG	GAT	ATC	ACC	TTT	TTC	CCT	TTT	GAT	CAT	CAA	652	
Lys	Ser	Ser	Cys	Pro	Met	Asp	Ile	Thr	Phe	Phe	Pro	Phe	Asp	His	Gln		
					160					165					170		
AAC	TGT	TCC	CTA	AAA	TTT	GGT	TCC	TGG	ACG	TAT	GAC	AAA	GCT	GAA	ATT	700	
Asn	Cys	Ser	Leu	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Lys	Ala	Glu	Ile		
				175					180					185			
GAT	CTT	CTA	ATC	ATT	GGA	TCA	AAA	GTG	GAT	ATG	AAT	GAT	TTT	TGG	GAA	748	
Asp	Leu	Leu	Ile	Ile	Gly	Ser	Lys	Val	Asp	Met	Asn	Asp	Phe	Trp	Glu		
			190					195					200				
AAC	AGT	GAA	TGG	GAA	ATC	ATT	GAT	GCC	TCT	GGC	TAC	AAA	CAT	GAC	ATC	796	
Asn	Ser	Glu	Trp	Glu	Ile	Ile	Asp	Ala	Ser	Gly	Tyr	Lys	His	Asp	Ile		
		205					210					215					
AAA	TAC	AAC	TGT	TGT	GAA	GAG	ATA	TAC	ACA	GAT	ATA	ACC	TAT	TCT	TTC	844	
Lys	Tyr	Asn	Cys	Cys	Glu	Glu	Ile	Tyr	Thr	Asp	Ile	Thr	Tyr	Ser	Phe		
			220			225					230						
TAC	ATT	AGA	AGA	TTG	CCG	ATG	TTT	TAC	ACG	ATT	AAT	CTG	ATC	ATC	CCT	892	
Tyr	Ile	Arg	Arg	Leu	Pro	Met	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro		
					240					245					250		
TGT	CTC	TTT	ATT	TCA	TTT	CTA	ACC	GTG	TTG	GTC	TTT	TAC	CTT	CCT	TCG	940	
Cys	Leu	Phe	Ile	Ser	Phe	Leu	Thr	Val	Leu	Val	Phe	Tyr	Leu	Pro	Ser		
				255					260					265			
GAC	TGT	GGT	GAA	AAA	GTG	ACG	CTT	TGT	ATT	TCA	GTC	CTG	CTT	TCT	CTG	988	
Asp	Cys	Gly	Glu	Lys	Val	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ser	Leu		
			270					275					280				

ACT GTG TTT TTG CTG GTC ATC ACA GAA ACC ATC CCA TCC ACA TCT CTG	1036
Thr Val Phe Leu Leu Val Ile Thr Glu Thr Ile Pro Ser Thr Ser Leu	
285 290 295	
GTG GTC CCA CTG GTG GGT GAG TAC CTG CTG TTC ACC ATG ATC TTT GTC	1084
Val Val Pro Leu Val Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val	
300 305 310	
ACA CTG TCC ATC GTG GTG ACT GTG TTT GTG TTG AAC ATA CAC TAC CGC	1132
Thr Leu Ser Ile Val Val Thr Val Phe Val Leu Asn Ile His Tyr Arg	
315 320 325 330	
ACC CCA ACC ACG CAC ACA ATG CCC AGG TGG GTG AAG ACA GTT TTC CTG	1180
Thr Pro Thr Thr His Thr Met Pro Arg Trp Val Lys Thr Val Phe Leu	
335 340 345	
AAG CTG CTG CCC CAG GTC CTG CTG ATG AGG TGG CCT CTG GAC AAG ACA	1228
Lys Leu Leu Pro Gln Val Leu Leu Met Arg Trp Pro Leu Asp Lys Thr	
350 355 360	
AGG GGC ACA GGC TCT GAT GCA GTG CCC AGA GGC CTT GCC AGG AGG CCT	1276
Arg Gly Thr Gly Ser Asp Ala Val Pro Arg Gly Leu Ala Arg Arg Pro	
365 370 375	
GCC AAA GGC AAG CTT GCA AGC CAT GGG GAA CCC AGA CAT CTT AAA GAA	1324
Ala Lys Gly Lys Leu Ala Ser His Gly Glu Pro Arg His Leu Lys Glu	
380 385 390	
TGC TTC CAT TGT CAC AAA CCA AAT GAG CTT GCC ACA AGC AAG AGA AGA	1372
Cys Phe His Cys His Lys Ser Asn Glu Leu Ala Thr Ser Lys Arg Arg	
395 400 405 410	
TTA AGT CAT CAG CCA TTA CAG TGG GTG GTG GAA AAT TCG GAG CAC TCG	1420
Leu Ser His Gln Pro Leu Gln Trp Val Val Glu Asn Ser Glu His Ser	
415 420 425	
CCT GAA GTT GAA GAT GTG ATT AAC AGT GTT CAG TTC ATA GCA GAA AAC	1468
Pro Glu Val Glu Asp Val Ile Asn Ser Val Gln Phe Ile Ala Glu Asn	
430 435 440	
ATG AAG AGC CAC AAT GAA ACC AAG GAG GTA GAA GAT GAC TGG AAA TAC	1516
Met Lys Ser His Asn Glu Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr	
445 450 455	
GTG GCC ATG GTG GTG GAC AGA GTA TTT CTT TGG GTA TTT ATA ATT GTC	1564
Val Ala Met Val Val Asp Arg Val Phe Leu Trp Val Phe Ile Ile Val	
460 465 470	
TGT GTA TTT GGA ACT GCA GGG CTA TTT CTA CAG CCA CTA CTT GGG AAC	1612
Cys Val Phe Gly Thr Ala Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn	
475 480 485 490	
ACA GGA AAA TCT TAAAATGTAT TTTCTTTTAT GTTCAGAAAT TTACAGACAC	1664
Thr Gly Lys Ser	
495	
CATATTTGTT CTGCATTCCC TGCCACAAGG AAAGGAAAGC AAAGGCTTCC CACCCAAGTC	1724
CCCCATCTGC TAAAACCCG	1743

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Leu Thr Ser Lys Gly Gln Gly Phe Leu His Gly Gly Leu Cys Leu
 1           5           10           15
Trp Leu Cys Val Phe Thr Pro Phe Phe Lys Gly Cys Val Gly Cys Ala
          20           25           30
Thr Glu Glu Arg Leu Phe His Lys Leu Phe Ser His Tyr Asn Gln Phe
          35           40           45
Ile Arg Pro Val Glu Asn Val Ser Asp Pro Val Thr Val His Phe Glu
          50           55           60
Val Ala Ile Thr Gln Leu Ala Asn Val Asp Glu Val Asn Gln Ile Met
          65           70           75           80
Glu Thr Asn Leu Trp Leu Arg His Ile Trp Asn Asp Tyr Lys Leu Arg
          85           90           95
Trp Asp Pro Met Glu Tyr Asp Gly Ile Glu Thr Leu Arg Val Pro Ala
          100          105          110
Asp Lys Ile Trp Lys Pro Asp Ile Val Leu Tyr Asn Asn Ala Val Gly
          115          120          125
Asp Phe Gln Val Glu Gly Lys Thr Lys Ala Leu Leu Lys Tyr Asn Gly
          130          135          140
Met Ile Thr Trp Thr Pro Pro Ala Ile Phe Lys Ser Ser Cys Pro Met
          145          150          155          160
Asp Ile Thr Phe Phe Pro Phe Asp His Gln Asn Cys Ser Leu Lys Phe
          165          170          175
Gly Ser Trp Thr Tyr Asp Lys Ala Glu Ile Asp Leu Leu Ile Ile Gly
          180          185          190
Ser Lys Val Asp Met Asn Asp Phe Trp Glu Asn Ser Glu Trp Glu Ile
          195          200          205
Ile Asp Ala Ser Gly Tyr Lys His Asp Ile Lys Tyr Asn Cys Cys Glu
          210          215          220
Glu Ile Tyr Thr Asp Ile Thr Tyr Ser Phe Tyr Ile Arg Arg Leu Pro
          225          230          235          240
Met Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Phe Ile Ser Phe
          245          250          255
Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Val
          260          265          270

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Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Val
  275                                280                                285
Ile Thr Glu Thr Ile Pro Ser Thr Ser Leu Val Val Pro Leu Val Gly
  290                                295                                300
Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val Val
  305                                310                                315                                320
Thr Val Phe Val Leu Asn Ile His Tyr Arg Thr Pro Thr Thr His Thr
  325                                330                                335
Met Pro Arg Trp Val Lys Thr Val Phe Leu Lys Leu Leu Pro Gln Val
  340                                345                                350
Leu Leu Met Arg Trp Pro Leu Asp Lys Thr Arg Gly Thr Gly Ser Asp
  355                                360                                365
Ala Val Pro Arg Gly Leu Ala Arg Arg Pro Ala Lys Gly Lys Leu Ala
  370                                375                                380
Ser His Gly Glu Pro Arg His Leu Lys Glu Cys Phe His Cys His Lys
  385                                390                                395                                400
Ser Asn Glu Leu Ala Thr Ser Lys Arg Arg Leu Ser His Gln Pro Leu
  405                                410                                415
Gln Trp Val Val Glu Asn Ser Glu His Ser Pro Glu Val Glu Asp Val
  420                                425                                430
Ile Asn Ser Val Gln Phe Ile Ala Glu Asn Met Lys Ser His Asn Glu
  435                                440                                445
Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr Val Ala Met Val Val Asp
  450                                455                                460
Arg Val Phe Leu Trp Val Phe Ile Ile Val Cys Val Phe Gly Thr Ala
  465                                470                                475                                480
Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn Thr Gly Lys Ser
  485                                490

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..1581
- (D) OTHER INFORMATION: /product= "ALPHA-7 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGCAGGC	GCAGGCCCGG	GCGACAGCCG	AGACGTGGAG	CGCGCCGGCT	CGCTGCAGCT	60
CCGGGACTCA	ACATGCGCTG	CTCGCCGGGA	GGCGTCTGGC	TGGCGCTGGC	CGCGTCGCTC	120
CTGCACGTGT	CCCTGCAAGG	CGAGTTCCAG	AGGAAGCTTT	ACAAGGAGCT	GGTCAAGAAC	180
TACAATCCCT	TGGAGAGGCC	CGTGGCCAAT	GACTCGCAAC	CACTCACCGT	CTACTTCTCC	240
CTGAGCCTCC	TGCAGATCAT	GGACGTGGAT	GAGAAGAACC	AAGTTTAAAC	CACCAACATT	300
TGGCTGCAAA	TGTCTTGGAC	AGATCACTAT	TTACAGTGGG	ATGTGTCAGA	ATATCCAGGG	360
GTGAAGACTG	TTCGTTTCCC	AGATGGCCAG	ATTTGGAAAC	CAGACATTCT	TCTCTATAAC	420
AGTGCTGATG	AGCGCTTTGA	CGCCACATTC	CACACTAACG	TGTTGGTGAA	TTCTTCTGGG	480
CATTGCCAGT	ACCTGCCTCC	AGGCATATTC	AAGAGTTCCT	GCTACATCGA	TGTACGCTGG	540
TTTCCCTTTG	ATGTGCAGCA	CTGCAAACCTG	AAGTTTGGGT	CCTGGTCTTA	CGGAGGCTGG	600
TCCTTGGATC	TGCAGATGCA	GGAGGCAGAT	ATCAGTGGCT	ATATCCCCAA	TGGAGAATGG	660
GACCTAGTGG	GAATCCCCGG	CAAGAGGAGT	GAAAGGTTCT	ATGAGTGCTG	CAAAGAGCCC	720
TACCCCGATG	TCACCTTCAC	AGTGACCATG	CGCCGCAGGA	CGCTCTACTA	TGGCCTCAAC	780
CTGCTGATCC	CCTGTGTGCT	CATCTCCGCC	CTCGCCCTGC	TGGTGTTCCT	GCTTCCTGCA	840
GATTCCGGGG	AGAAGATTTC	CCTGGGGATA	ACAGTCTTAC	TCTCTCTTAC	CGTCTTCATG	900
CTGCTCGTGG	CTGAGATCAT	GCCCGCAACA	TCCGATTCGG	TACCATTGAT	AGCCCAGTAC	960
TTGCCAGCA	CCATGATCAT	CGTGGGCCTC	TCGGTGGTGG	TGACGGTGAT	CGTGCTGCAG	1020
TACCACCACC	ACGACCCCGA	CGGGGGCAAG	ATGCCCAAGT	GGACCAGAGT	CATCCTTCTG	1080
AACTGGTGCG	CGTGGTTCCT	SCGAATGAAG	AGGCCCGGGG	AGGACAAGGT	GCGCCCGGCC	1140
TGCCAGCACA	AGCAGCGGCG	CTGCAGCCTG	GCCAGTGTGG	AGATGAGCGC	CGTGGCGCCG	1200
CCGCCCCGCA	GCAACGGGAA	CCTGCTGTAC	ATCGGCTTCC	GCGGCCTGGA	CGGCGTGCAC	1260
TGTGTCCCGA	CCCCCGACTC	TGGGGTAGTG	TGTGGCCGCA	TGGCCTGCTC	CCCCACGCAC	1320
GATGAGCACC	TCCTGCACGG	CGGGCAACCC	CCCAGGGGGG	ACCCGGACTT	GGCCAAGATC	1380
CTGGAGGAGG	TCCGCTACAT	TGCCAATCGC	TTCCGCTGCC	AGGACGAAAG	CGAGGCGGTC	1440
TGCAGCGAGT	GGAAGTTCGC	CGCCTGTGTG	GTGGACCGCC	TGTGCCTCAT	GGCCTTCTCG	1500
GTCTTCACCA	TCATCTGCAC	CATCGGCATC	CTGATGTCGG	CTCCCAACTT	CGTGGAGGCC	1560
GTGTCCAAAG	ACTTTGCGTA	ACCACGCCTG	GTTCTGTACA	TGTGGAAAAC	TCACAGATGG	1620
GCAAGGCCCT	TGGCTTGGCG	AGATTTGGGG	GTGCTAATCC	AGGACAGCAT	TACACGCCAC	1680
AACTCCAGTG	TTCCCTTCTG	GCTGTCAGTC	GTGTTGCTTA	CGGTTTCTTT	GTTACTTTAG	1740
GTAGTAGAAT	CTCAGCACTT	TGTTTCATAT	TCTCAGATGG	GCTGATAGAT	ATCCTTGGCA	1800
CATCCGTACC	ATCGGTCAGC	AGGGCCACTG	AGTAGTCATT	TTGCCCATTA	GCCCACTGCC	1860

TGGAAAGCCC TTCGGA

1876

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
 1 5 10 15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
 20 25 30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
 35 40 45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
 50 55 60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
 65 70 75 80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
 85 90 95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
 100 105 110

Leu L yr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
 115 120 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
 130 135 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
 145 150 155 160

Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
 165 170 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
 180 185 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
 195 200 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
 210 215 220

Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro
 225 230 235 240

Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala

245										250					255				
Asp	Ser	Gly	Glu	Lys	Ile	Ser	Leu	Gly	Ile	Thr	Val	Leu	Leu	Ser	Leu				
			260					265					270						
Thr	Val	Phe	Met	Leu	Leu	Val	Ala	Glu	Ile	Met	Pro	Ala	Thr	Ser	Asp				
		275					280					285							
Ser	Val	Pro	Leu	Ile	Ala	Gln	Tyr	Phe	Ala	Ser	Thr	Met	Ile	Ile	Val				
	290					295					300								
Gly	Leu	Ser	Val	Val	Val	Thr	Val	Ile	Val	Leu	Gln	Tyr	His	His	His				
305					310					315					320				
Asp	Pro	Asp	Gly	Gly	Lys	Met	Pro	Lys	Trp	Thr	Arg	Val	Ile	Leu	Leu				
				325					330					335					
Asn	Trp	Cys	Ala	Trp	Phe	Leu	Arg	Met	Lys	Arg	Pro	Gly	Glu	Asp	Lys				
			340					345					350						
Val	Arg	Pro	Ala	Cys	Gln	His	Lys	Gln	Arg	Arg	Cys	Ser	Leu	Ala	Ser				
		355					360					365							
Val	Glu	Met	Ser	Ala	Val	Ala	Pro	Pro	Pro	Ala	Ser	Asn	Gly	Asn	Leu				
	370					375					380								
Leu	Tyr	Ile	Gly	Phe	Arg	Gly	Leu	Asp	Gly	Val	His	Cys	Val	Pro	Thr				
385					390					395					400				
Pro	Asp	Ser	Gly	Val	Val	Cys	Gly	Arg	Met	Ala	Cys	Ser	Pro	Thr	His				
				405				410						415					
Asp	Glu	His	Leu	Leu	His	Gly	Gly	Gln	Pro	Pro	Glu	Gly	Asp	Pro	Asp				
			420					425					430						
Leu	Ala	Lys	Ile	Leu	Glu	Glu	Val	Arg	Tyr	Ile	Ala	Asn	Arg	Phe	Arg				
		435					440					445							
Cys	Gln	Asp	Glu	Ser	Glu	Ala	Val	Cys	Ser	Glu	Trp	Lys	Phe	Ala	Ala				
	450					455					460								
Cys	Val	Val	Asp	Arg	Leu	Cys	Leu	Met	Ala	Phe	Ser	Val	Phe	Thr	Ile				
465					470					475					480				
Ile	Cys	Thr	Ile	Gly	Ile	Leu	Met	Ser	Ala	Pro	Asn	Phe	Val	Glu	Ala				
				485				490						495					
Val	Ser	Lys	Asp	Phe	Ala														
			500																

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 265..1773

(D) OTHER INFORMATION: /product= "BETA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCTCCCCC TCACCGTCCC AATTGTATTC CCTGGAAGAG CAGCCGGAAA AGCCTCCGCC	60
TGCTCATACC AGGATAGGCA AGAAGCTGGT TTCTCCTCGC AGCCGGCTCC CTGAGGCCCA	120
GGAACCACCG CGGCGGCCGG CACCACCTGG ACCCAGCTCC AGGCGGGCGC GGCTTCAGCA	180
CCACGGACAG CGCCCCACCC GCGGCCCTCC CCCC GGCGGC GCGCTCCAGC CGGTGTAGGC	240
GAGGCAGCGA GCTATGCCCG CGGC ATG GCC CGG CGC TGC GGC CCC GTG GCG	291
Met Ala Arg Arg Cys Gly Pro Val Ala	
1 5	
CTG CTC CTT GGC TTC GGC CTC CTC CGG CTG TGC TCA GGG GTG TGG GGT	339
Leu Leu Leu Gly Phe Gly Leu Leu Arg Leu Cys Ser Gly Val Trp Gly	
10 15 20 25	
ACG GAT ACA GAG GAG CGG CTG GTG GAG CAT CTC CTG GAT CCT TCC CGC	387
Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg	
30 35 40	
TAC AAC AAG CTT ATC CGC CCA GCC ACC AAT GGC TCT GAG CTG GTG ACA	435
Tyr Asn Lys Leu Ile Arg Pro Ala Thr Asn Gly Ser Glu Leu Val Thr	
45 50 55	
GTA CAG CTT ATG GTG TCA CTG GCC CAG CTC ATC AGT GTG CAT GAG CGG	483
Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu Arg	
60 65 70	
GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT	531
Glu Gln Ile Met Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp	
75 80 85	
TAT CGC CTC ACC TGG AAG CCT GAA GAG TTT GAC AAC ATG AAG AAA GTT	579
Tyr Arg Leu Thr Trp Lys Pro Glu Glu Phe Asp Asn Met Lys Lys Val	
90 95 100 105	
CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTC CTG TAC AAC	627
Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn	
110 115 120	
AAT GCT GAC GGC ATG TAC GAG GTG TCC TTC TAT TCC AAT GCC GTG GTC	675
Asn Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val	
125 130 135	
TCC TAT GAT GGC AGC ATC TTC TGG CTG CCG CCT GCC ATC TAC AAG AGC	723
Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro Pro Ala Ile Tyr Lys Ser	
140 145 150	
GCA TGC AAG ATT GAA GTA AAG CAC TTC CCA TTT GAC CAG CAG AAC TGC	771
Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys	
155 160 165	
ACC ATG AAG TTC CGT TCG TGG ACC TAC GAC CGC ACA GAG ATC GAC TTG	819
Thr Met Lys Phe Arg Ser Trp Thr Tyr Asp Arg Thr Glu Ile Asp Leu	

170					175					180					185	
GTG	CTG	AAG	AGT	GAG	GTG	GCC	AGC	CTG	GAC	GAC	TTC	ACA	CCT	AGT	GGT	867
Val	Leu	Lys	Ser	Glu	Val	Ala	Ser	Leu	Asp	Asp	Phe	Thr	Pro	Ser	Gly	
				190					195					200		
GAG	TGG	GAC	ATC	GTG	GCG	CTG	CCG	GGC	CGG	CGC	AAC	GAG	AAC	CCC	GAC	915
Glu	Trp	Asp	Ile	Val	Ala	Leu	Pro	Gly	Arg	Arg	Asn	Glu	Asn	Pro	Asp	
			205					210					215			
GAC	TCT	ACG	TAC	GTG	GAC	ATC	ACG	TAT	GAC	TTC	ATC	ATT	CGC	CGC	AAG	963
Asp	Ser	Thr	Tyr	Val	Asp	Ile	Thr	Tyr	Asp	Phe	Ile	Ile	Arg	Arg	Lys	
		220					225					230				
CCG	CTC	TTC	TAC	ACC	ATC	AAC	CTC	ATC	ATC	CCC	TGT	GTG	CTC	ATC	ACC	1011
Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Val	Leu	Ile	Thr	
	235					240				245						
TCG	CTA	GCC	ATC	CTT	GTC	TTC	TAC	CTG	CCA	TCC	GAC	TGT	GGC	GAG	AAG	1059
Ser	Leu	Ala	Ile	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Asp	Cys	Gly	Glu	Lys	
250					255					260					265	
ATG	ACG	TTG	TGC	ATC	TCA	GTG	CTG	CTG	GCG	CTC	ACG	GTC	TTC	CTG	CTG	1107
Met	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ala	Leu	Thr	Val	Phe	Leu	Leu	
				270					275					280		
CTC	ATC	TCC	AAG	ATC	GTG	CCT	CCC	ACC	TCC	CTC	GAC	GTG	CCG	CTC	GTC	1155
Leu	Ile	Ser	Lys	Ile	Val	Pro	Pro	Thr	Ser	Leu	Asp	Val	Pro	Leu	Val	
			285					290					295			
GGC	AAG	TAC	CTC	ATG	TTC	ACC	ATG	GTG	CTT	GTC	ACC	TTC	TCC	ATC	GTC	1203
Gly	Lys	Tyr	Leu	Met	Phe	Thr	Met	Val	Leu	Val	Thr	Phe	Ser	Ile	Val	
		300					305					310				
ACC	AGC	GTG	TGC	GTG	CTC	AAC	GTG	CAC	CAC	CGC	TCG	CCC	ACC	ACG	CAC	1251
Thr	Ser	Val	Cys	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Thr	Thr	His	
	315					320				325						
ACC	ATG	GCG	CCC	TGG	GTG	AAG	GTC	GTC	TTC	CTG	GAG	AAG	CTG	CCC	GCG	1299
Thr	Met	Ala	Pro	Trp	Val	Lys	Val	Val	Phe	Leu	Glu	Lys	Leu	Pro	Ala	
330					335					340					345	
CTG	CTC	TTC	ATG	CAG	CAG	CCA	CGC	CAT	CAT	TGC	GCC	CGT	CAG	CGC	CTG	1347
Leu	Leu	Phe	Met	Gln	Gln	Pro	Arg	His	His	Cys	Ala	Arg	Gln	Arg	Leu	
			350					355					360			
CGC	CTG	CGG	CGA	CGC	CAG	CGT	GAG	CGC	GAG	GGC	GCT	GGA	GCC	CTC	TTC	1395
Arg	Leu	Arg	Arg	Arg	Gln	Arg	Glu	Arg	Glu	Gly	Ala	Gly	Ala	Leu	Phe	
			365				370					375				
TTC	CGC	GAA	GCC	CCA	GGG	GCC	GAC	TCC	TGC	ACG	TGC	TTC	GTC	AAC	CGC	1443
Phe	Arg	Glu	Ala	Pro	Gly	Ala	Asp	Ser	Cys	Thr	Cys	Phe	Val	Asn	Arg	
		380					385					390				
GCG	TCG	GTG	CAG	GGG	TTG	GCC	GGG	GCC	TTC	GGG	GCT	GAG	CCT	GCA	CCA	1491
Ala	Ser	Val	Gln	Gly	Leu	Ala	Gly	Ala	Phe	Gly	Ala	Glu	Pro	Ala	Pro	
	395				400					405						
GTG	GCG	GGC	CCC	GGG	CGC	TCA	GGG	GAG	CCG	TGT	GGC	TGT	GGC	CTC	CGG	1539
Val	Ala	Gly	Pro	Gly	Arg	Ser	Gly	Glu	Pro	Cys	Gly	Cys	Gly	Leu	Arg	
410					415					420					425	

GAG GCG GTG GAC GGC GTG CGC TTC ATC GCA GAC CAC ATG CGG AGC GAG	1587
Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu	
430 435 440	
GAC GAT GAC CAG AGC GTG AGT GAG GAC TGG AAG TAC GTC GCC ATG GTG	1635
Asp Asp Asp Gln Ser Val Ser Glu Asp Trp Lys Tyr Val Ala Met Val	
445 450 455	
ATC GAC CGC CTC TTC CTC TGG ATC TTT GTC TTT GTC TGT GTC TTT GGC	1683
Ile Asp Arg Leu Phe Leu Trp Ile Phe Val Phe Val Cys Val Phe Gly	
460 465 470	
ACC ATC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACC ACC ACC	1731
Thr Ile Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Thr Thr	
475 480 485	
ACC TTC CTC CAC TCA GAC CAC TCA GCC CCC AGC TCC AAG TGAGGCCCTT	1780
Thr Phe Leu His Ser Asp His Ser Ala Pro Ser Ser Lys	
490 495 500	
CCTCATCTCC ATGCTCTTTC ACCCTGCCAC CCTCTGCTGC ACAGTAGTGT TGGGTGGAGG	1840
ATGGACGAGT GAGCTACCAG GAAGAGGGGC GCTGCCCCCA CAGATCCATC CTTTGTGCTTC	1900
ATCTGGAGTC CCTCCTCCCC CACGCCTCCA TCCACACACA GCAGCTCCAA CCTGGAGGCT	1960
GGACCAACTG CTTTGTTTTG GCTGCTCTCC ATCTCTTGTA CCAGCCCAGG CAATAGTGTT	2020
GAGGAGGGGA GCAAGGCTGC TAAGTGAAG ACAGAGATGG CAGAGCCATC CACCCTGAGG	2080
AGTGACGGGC AAGGGGCCAG GAAGGGGACA GGATTGTCTG CTGCCTCCAA GTCATGGGAG	2140
AAGAGGGGTA TAGGACAAGG GGTGGAAGGG CAGGAGCTCA CACCGCACCG GGCTGGCCTG	2200
ACACAATGGT AGCTCTGAAG GGAGGGGAAG AGAGAGGCCT GGGTGTGACC TGACACCTGC	2260
CGTGCTTGA GTGGACAGCA GCTGGACTGG GTGGGCCCCA CAGTGGTCAG CGATTCTTGC	2320
CAAGTAGGGT TTAGCCGGGC CCCATGGTCA CAGACCCCTG GGGGAGGCTT CCAGCTCAGT	2380
CCCACAGCCC CTTGCTTCTA AGGGATCCAG AGACCTGCTC CAGATCCTCT TTCCCCACTG	2440
AAGAATTC	2448

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Arg	Arg	Cys	Gly	Pro	Val	Ala	Leu	Leu	Leu	Gly	Phe	Gly	Leu
1				5					10					15	
Leu	Arg	Leu	Cys	Ser	Gly	Val	Trp	Gly	Thr	Asp	Thr	Glu	Glu	Arg	Leu
			20					25					30		

Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg Pro
 35 40 45
 Ala Thr Asn Gly Ser Glu Leu Val Thr Val Gln Leu Met Val Ser Leu
 50 55 60
 Ala Gln Leu Ile Ser Val His Glu Arg Glu Gln Ile Met Thr Thr Asn
 65 70 75 80
 Val Trp Leu Thr Gln Glu Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro
 85 90 95
 Glu Glu Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile
 100 105 110
 Trp Leu Pro Asp Val Val Leu Tyr Asn Asn Ala Asp Gly Met Tyr Glu
 115 120 125
 Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe
 130 135 140
 Trp Leu Pro Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys
 145 150 155 160
 His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Arg Ser Trp
 165 170 175
 Thr Tyr Asp Arg Thr Glu Ile Asp Leu Val Leu Lys Ser Glu Val Ala
 180 185 190
 Ser Leu Asp Asp Phe Thr Pro Ser Gly Glu Trp Asp Ile Val Ala Leu
 195 200 205
 Pro Gly Arg Arg Asn Glu Asn Pro Asp Asp Ser Thr Tyr Val Asp Ile
 210 215 220
 Thr Tyr Asp Phe Ile Ile Arg Arg Lys Pro Leu Phe Tyr Thr Ile Asn
 225 230 235 240
 Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe
 245 250 255
 Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Leu Cys Ile Ser Val
 260 265 270
 Leu Leu Ala Leu Thr Val Phe Leu Leu Leu Ile Ser Lys Ile Val Pro
 275 280 285
 Pro Thr Ser Leu Asp Val Pro Leu Val Gly Lys Tyr Leu Met Phe Thr
 290 295 300
 Met Val Leu Val Thr Phe Ser Ile Val Thr Ser Val Cys Val Leu Asn
 305 310 315 320
 Val His His Arg Ser Pro Thr Thr His Thr Met Ala Pro Trp Val Lys
 325 330 335
 Val Val Phe Leu Glu Lys Leu Pro Ala Leu Leu Phe Met Gln Gln Pro
 340 345 350
 Arg His His Cys Ala Arg Gln Arg Leu Arg Leu Arg Arg Arg Gln Arg

355		360		365
Glu Arg Glu Gly Ala Gly Ala Leu Phe Phe Arg Glu Ala Pro Gly Ala				
370		375		380
Asp Ser Cys Thr Cys Phe Val Asn Arg Ala Ser Val Gln Gly Leu Ala				
385		390		400
Gly Ala Phe Gly Ala Glu Pro Ala Pro Val Ala Gly Pro Gly Arg Ser				
	405		410	415
Gly Glu Pro Cys Gly Cys Gly Leu Arg Glu Ala Val Asp Gly Val Arg				
	420		425	430
Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Ser				
	435		440	445
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp				
	450		455	460
Ile Phe Val Phe Val Cys Val Phe Gly Thr Ile Gly Met Phe Leu Gln				
465		470		480
Pro Leu Phe Gln Asn Tyr Thr Thr Thr Thr Phe Leu His Ser Asp His				
	485		490	495
Ser Ala Pro Ser Ser Lys				
	500			

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 98..1474
- (D) OTHER INFORMATION: /product= "BETA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGGAACCCC TGTATTTTCT TTTCAAACCC CCCTTTTCCA GTGGAAATGC TCTGTTGTTA	60
AAAAGGAAGA AACTGTCTTT CTGAACTGA CATCACG ATG CTC CCA GAT TTT ATG	115
Met Leu Pro Asp Phe Met	
1 5	
CTG GTT CTC ATC GTC CTT GGC ATC CCT TCC TCA GCC ACC ACA GGT TTC	163
Leu Val Leu Ile Val Leu Gly Ile Pro Ser Ser Ala Thr Thr Gly Phe	
10 15 20	
AAC TCA ATC GCC GAA AAT GAA GAT GCC CTC CTC AGA CAT TTG TTC CAA	211
Asn Ser Ile Ala Glu Asn Glu Asp Ala Leu Leu Arg His Leu Phe Gln	
25 30 35	

GGT Gly	TAT Tyr	CAG Gln	AAA Lys	TGG Trp	GTC Val	CGC Arg	CCT Pro	GTA Val	TTA Leu	CAT His	TCT Ser	AAT Asn	GAC Asp	ACC Thr	ATA Ile	259
40						45					50					
AAA Lys	GTA Val	TAT Tyr	TTT Phe	GGA Gly	TTG Leu	AAA Lys	ATA Ile	TCC Ser	CAG Gln	CTT Leu	GTA Val	GAT Asp	GTG Val	GAT Asp	GAA Glu	307
55					60					65					70	
AAG Lys	AAT Asn	CAG Gln	CTG Leu	ATG Met	ACA Thr	ACC Thr	AAT Asn	GTG Val	TGG Trp	CTC Leu	AAA Lys	CAG Gln	GAA Glu	TGG Trp	ACA Thr	355
				75					80					85		
GAC Asp	CAC His	AAG Lys	TTA Leu	CGC Arg	TGG Trp	AAT Asn	CCT Pro	GAT Asp	GAT Asp	TAT Tyr	GGT Gly	GGG Gly	ATC Ile	CAT His	TCC Ser	403
			90					95					100			
ATT Ile	AAA Lys	GTT Val	CCA Pro	TCA Ser	GAA Glu	TCT Ser	CTG Leu	TGG Trp	CTT Leu	CCT Pro	GAC Asp	ATA Ile	GTT Val	CTC Leu	TTT Phe	451
		105					110					115				
GAA Glu	AAT Asn	GCT Ala	GAC Asp	GGC Gly	CGC Arg	TTC Phe	GAA Glu	GGC Gly	TCC Ser	CTG Leu	ATG Met	ACC Thr	AAG Lys	GTC Val	ATC Ile	499
		120				125					130					
GTG Val	AAA Lys	TCA Ser	AAC Asn	GGA Gly	ACT Thr	GTT Val	GTC Val	TGG Trp	ACC Thr	CCT Pro	CCC Pro	GCC Ala	AGC Ser	TAC Tyr	AAA Lys	547
135					140					145					150	
AGC Ser	TCC Ser	TGC Cys	ACC Thr	ATG Met	GAC Asp	GTC Val	ACG Thr	TTT Phe	TTC Phe	CCG Pro	TTC Phe	GAC Asp	CGA Arg	CAG Gln	AAC Asn	595
				155					160					165		
TGC Cys	TCC Ser	ATG Met	AAG Lys	TTT Phe	GGA Gly	TCC Ser	TGG Trp	ACT Thr	TAT Tyr	GAT Asp	GGC Gly	ACC Thr	ATG Met	GTT Val	GAC Asp	643
			170					175					180			
CTC Leu	ATT Ile	TTG Leu	ATC Ile	AAT Asn	GAA Glu	AAT Asn	GTC Val	GAC Asp	AGA Arg	AAA Lys	GAC Asp	TTC Phe	TTC Phe	GAT Asp	AAC Asn	691
		185					190					195				
GGA Gly	GAA Glu	TGG Trp	GAA Glu	ATA Ile	CTG Leu	AAT Asn	GCA Ala	AAG Lys	GGG Gly	ATG Met	AAG Lys	GGG Gly	AAC Asn	AGA Arg	AGG Arg	739
		200				205					210					
GAC Asp	GGC Gly	GTG Val	TAC Tyr	TCC Ser	TAT Tyr	CCC Pro	TTT Phe	ATC Ile	ACG Thr	TAT Tyr	TCC Ser	TTC Phe	GTC Val	CTG Leu	AGA Arg	787
215					220					225				230		
CGC Arg	CTG Leu	CCT Pro	TTA Leu	TTC Phe	TAT Tyr	ACC Thr	CTC Leu	TTT Phe	CTC Leu	ATC Ile	ATC Ile	CCC Pro	TGC Cys	CTG Leu	GGG Gly	835
				235					240					245		
CTG Leu	TCT Ser	TTC Phe	CTA Leu	ACA Thr	GTT Val	CTT Leu	GTG Val	TTC Phe	TAT Tyr	TTA Leu	CCT Pro	TCG Ser	GAT Asp	GAA Glu	GGA Gly	883
			250				255						260			
GAA Glu	AAA Lys	CTT Leu	TCA Ser	TTA Leu	TCC Ser	ACA Thr	TCG Ser	GTC Val	TTG Leu	GTT Val	TCT Ser	CTG Leu	ACA Thr	GTT Val	TTC Phe	931
		265					270					275				
CTT Leu	TTA Leu	GTG Val	ATT Leu	GAA Leu	GAA Leu	ATC Leu	ATC Leu	CCA Leu	TCG Leu	TCT Leu	TCC Leu	AAA Leu	GTC Leu	ATT Leu	CCT Leu	979

Leu	Leu	Val	Ile	Glu	Glu	Ile	Ile	Pro	Ser	Ser	Ser	Lys	Val	Ile	Pro	
280						285					290					
CTC	ATT	GGA	GAG	TAC	CTG	CTG	TTC	ATC	ATG	ATT	TTT	GTG	ACC	CTG	TCC	1027
Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Ile	Met	Ile	Phe	Val	Thr	Leu	Ser	
295					300					305					310	
ATC	ATT	GTT	ACC	GTG	TTT	GTC	ATT	AAC	GTT	CAC	CAC	AGA	TCT	TCT	TCC	1075
Ile	Ile	Val	Thr	Val	Phe	Val	Ile	Asn	Val	His	His	Arg	Ser	Ser	Ser	
				315					320					325		
ACG	TAC	CAC	CCC	ATG	GCC	CCC	TGG	GTT	AAG	AGG	CTC	TTT	CTG	CAG	AAA	1123
Thr	Tyr	His	Pro	Met	Ala	Pro	Trp	Val	Lys	Arg	Leu	Phe	Leu	Gln	Lys	
			330					335					340			
CTT	CCA	AAA	TTA	CTT	TGC	ATG	AAA	GAT	CAT	GTG	GAT	CGC	TAC	TCA	TCC	1171
Leu	Pro	Lys	Leu	Leu	Cys	Met	Lys	Asp	His	Val	Asp	Arg	Tyr	Ser	Ser	
		345					350					355				
CCA	GAG	AAA	GAG	GAG	AGT	CAA	CCA	GTA	GTG	AAA	GGC	AAA	GTC	CTC	GAA	1219
Pro	Glu	Lys	Glu	Glu	Ser	Gln	Pro	Val	Val	Lys	Gly	Lys	Val	Leu	Glu	
	360					365					370					
AAA	AAG	AAA	CAG	AAA	CAG	CTT	AGT	GAT	GGA	GAA	AAA	GTT	CTA	GTT	GCT	1267
Lys	Lys	Lys	Gln	Lys	Gln	Leu	Ser	Asp	Gly	Glu	Lys	Val	Leu	Val	Ala	
375					380					385					390	
TTT	TTG	GAA	AAA	GCT	GCT	GAT	TCC	ATT	AGA	TAC	ATT	TCC	AGA	CAT	GTG	1315
Phe	Leu	Glu	Lys	Ala	Ala	Asp	Ser	Ile	Arg	Tyr	Ile	Ser	Arg	His	Val	
				395					400					405		
AAG	AAA	GAA	CAT	TTT	ATC	AGC	CAG	GTA	GTA	CAA	GAC	TGG	AAA	TTT	GTA	1363
Lys	Lys	Glu	His	Phe	Ile	Ser	Gln	Val	Val	Gln	Asp	Trp	Lys	Phe	Val	
			410					415					420			
GCT	CAA	GTT	CTT	GAC	CGA	ATC	TTC	CTG	TGG	CTC	TTT	CTG	ATA	GTG	TCA	1411
Ala	Gln	Val	Leu	Asp	Arg	Ile	Phe	Leu	Trp	Leu	Phe	Leu	Ile	Val	Ser	
		425					430					435				
GCA	ACA	GGC	TCG	GTT	CTG	ATT	TTT	ACC	CCT	GCT	TTG	AAG	ATG	TGG	CTA	1459
Ala	Thr	Gly	Ser	Val	Leu	Ile	Phe	Thr	Pro	Ala	Leu	Lys	Met	Trp	Leu	
	440					445					450					
CAT	AGT	TAC	CAT	TAGGAATTTT AAAAGACATA AGTACTAAAT TACACCTTAG												1511
His	Ser	Tyr	His													
455																
ACCTGACATC TGGCTATCAC ACAGACAGAA TCCAAATGCA TGTGCTTGTT CTACGAACCC																1571
CGAATGCGTT GTCTTTGTGG AAATGGAACA TCTCCTCATG GGAGAACTC TGGTAAATGT																1631
GCTCATTTGT GGTGCCATG AGAGTGAGCT GCTTTTAAAG AAAGTGGAGC CTCCTCAGAC																1691
CCCTGCCTTG GCTTCCCGAG ACATTCAGGG AGGGATCATA GGTCCAGGCT TGAGCTCACA																1751
TGTGGCCAGA GTGACAAAA AGCTGTTGCT ACTTGGTGGA GGAACACCTC CTAGAAGCAG																1811
CAGGCCCTCGG TGGTGGGGGA GGGGGGATTC ACCTGGAATT AAGGAAGTCT CGGTGTCGAG																1871
CTATCTGTGT GGGCAGAGCC TGGATCTCCC ACCCTGCACT GGCCTCCTTG GTGCCG																1927

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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Met Leu Pro Asp Phe Met Leu Val Leu Ile Val Leu Gly Ile Pro Ser
 1           5           10           15
Ser Ala Thr Thr Gly Phe Asn Ser Ile Ala Glu Asn Glu Asp Ala Leu
          20           25           30
Leu Arg His Leu Phe Gln Gly Tyr Gln Lys Trp Val Arg Pro Val Leu
          35           40           45
His Ser Asn Asp Thr Ile Lys Val Tyr Phe Gly Leu Lys Ile Ser Gln
          50           55           60
Leu Val Asp Val Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp
          65           70           75           80
Leu Lys Gln Glu Trp Thr Asp His Lys Leu Arg Trp Asn Pro Asp Asp
          85           90           95
Tyr Gly Gly Ile His Ser Ile Lys Val Pro Ser Glu Ser Leu Trp Leu
          100          105          110
Pro Asp Ile Val Leu Phe Glu Asn Ala Asp Gly Arg Phe Glu Gly Ser
          115          120          125
Leu Met Thr Lys Val Ile Val Lys Ser Asn Gly Thr Val Val Trp Thr
          130          135          140
Pro Pro Ala Ser Tyr Lys Ser Ser Cys Thr Met Asp Val Thr Phe Phe
          145          150          155          160
Pro Phe Asp Arg Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr
          165          170          175
Asp Gly Thr Met Val Asp Leu Ile Leu Ile Asn Glu Asn Val Asp Arg
          180          185          190
Lys Asp Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Lys Gly
          195          200          205
Met Lys Gly Asn Arg Arg Asp Gly Val Tyr Ser Tyr Pro Phe Ile Thr
          210          215          220
Tyr Ser Phe Val Leu Arg Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu
          225          230          235          240
Ile Ile Pro Cys Leu Gly Leu Ser Phe Leu Thr Val Leu Val Phe Tyr
          245          250          255
Leu Pro Ser Asp Glu Gly Glu Lys Leu Ser Leu Ser Thr Ser Val Leu
          260          265          270

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Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser
 275 280 285
 Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met
 290 295 300
 Ile Phe Val Thr Leu Ser Ile Ile Val Thr Val Phe Val Ile Asn Val
 305 310 315 320
 His His Arg Ser Ser Ser Thr Tyr His Pro Met Ala Pro Trp Val Lys
 325 330 335
 Arg Leu Phe Leu Gln Lys Leu Pro Lys Leu Leu Cys Met Lys Asp His
 340 345 350
 Val Asp Arg Tyr Ser Ser Pro Glu Lys Glu Glu Ser Gln Pro Val Val
 355 360 365
 Lys Gly Lys Val Leu Glu Lys Lys Lys Gln Lys Gln Leu Ser Asp Gly
 370 375 380
 Glu Lys Val Leu Val Ala Phe Leu Glu Lys Ala Ala Asp Ser Ile Arg
 385 390 395 400
 Tyr Ile Ser Arg His Val Lys Lys Glu His Phe Ile Ser Gln Val Val
 405 410 415
 Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp
 420 425 430
 Leu Phe Leu Ile Val Ser Ala Thr Gly Ser Val Leu Ile Phe Thr Pro
 435 440 445
 Ala Leu Lys Met Trp Leu His Ser Tyr His
 450 455

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..1583
- (D) OTHER INFORMATION: /product= "BETA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGCGCTCA CTCGACCGCG CGGCTCACGG GTGCCCTGTG ACCCCACAGC GGAGCTCGCG	60
GCGGCTGCCA CCCGGCCCCG CCGGCCATGA GGCGCGCGCC TTCCCTGGTC CTTTCTCTCC	120
TGGTCGCCCT TTGCGGGCGC GGGAAGTACC GCGTGGCCAA TGCGGAGGAA AAGCTGATGG	180

ACGACCTTCT	GAACAAAACC	CGTTACAATA	ACCTGATCCG	CCCAGCCACC	AGCTCCTCAC	240
AGCTCATCTC	CATCAAGCTG	CAGCTCTCCC	TGGCCCAGCT	TATCAGCGTG	AATGAGCGAG	300
AGCAGATCAT	GACCACCAAT	GTCTGGCTGA	AACAGGAATG	GACTGATTAC	CGCCTGACCT	360
GGAACAGCTC	CCGCTACGAG	GGTGTGAACA	TCCTGAGGAT	CCCTGCAAAG	CGCATCTGGT	420
TGCCTGACAT	CGTGCTTTAC	AACAACGCCG	ACGGGACCTA	TGAGGTGTCT	GTCTACACCA	480
ACTTGATAGT	CCGGTCCAAC	GGCAGCGTCC	TGTGGCTGCC	CCCTGCCATC	TACAAGAGCG	540
CCTGCAAGAT	TGAGGTGAAG	TACTTTCCCT	TCGACCAGCA	GAAGTGCACC	CTCAAGTTCC	600
GCTCCTGGAC	CTATGACCAC	ACGGAGATAG	ACATGGTCCT	CATGACGCCC	ACAGCCAGCA	660
TGGATGACTT	TACTCCCAGT	GGTGAGTGGG	ACATAGTGGC	CCTCCCAGGG	AGAAGGACAG	720
TGAACCCACA	AGACCCCAGC	TACGTGGACG	TGACTTACGA	CTTCATCATC	AAGCGCAAGC	780
CTCTGTTCTA	CACCATCAAC	CTCATCATCC	CCTGCGTGCT	CACCACCTTG	CTGGCCATCC	840
TCGTCTTCTA	CCTGCCATCC	GACTGCGGCG	AGAAGATGAC	ACTGTGCATC	TCAGTGCTGC	900
TGGCACTGAC	ATTCTTCTTG	CTGCTCATCT	CCAAGATCGT	GCCACCCACC	TCCCTCGATG	960
TGCCTCTCAT	CGGCAAGTAC	CTCATGTTCA	CCATGGTGCT	GGTCACCTTC	TCCATCGTCA	1020
CCAGCGTCTG	TGTGCTCAAT	GTGCACCACC	GCTCGCCCAG	CACCCACACC	ATGGCACCCCT	1080
GGGTCAAGCG	CTGCTTCCCTG	CACAAGCTGC	CTACCTTCCT	CTTCATGAAG	CGCCCTGGCC	1140
CCGACAGCAG	CCCGGCCAGA	GCCTTCCCGC	CCAGCAAGTC	ATGCGTGACC	AAGCCCGAGG	1200
CCACCGCCAC	CTCCACCAGC	CCCTCCAAC	TCTATGGGAA	CTCCATGTAC	TTTGTGAACC	1260
CCGCCTCTGC	AGCTTCCAAG	TCTCCAGCCG	GCTCTACCCC	GGTGGCTATC	CCCAGGGATT	1320
TCTGGCTGCG	GTCCTCTGGG	AGGTTCGAC	AGGATGTGCA	GGAGGCATTA	GAAGGTGTCA	1380
GCTTCATCGC	CCAGCACATG	AAGAATGACG	ATGAAGACCA	GAGTGTGCTT	GAGGACTGGA	1440
AGTACGTGGC	TATGGTGGTG	GACCGGCTGT	TCCTGTGGGT	GTTTCATGTTT	GTGTGCGTCC	1500
TGGGCACTGT	GGGGCTCTTC	CTGCCGCCCC	TCTTCCAGAC	CCATGCAGCT	TCTGAGGGGC	1560
CCTACGCTGC	CCAGCGTGAC	TGAGGGCCCC	CTGGGTGTG	GGGTGAGAGG	ATGTGAGTGG	1620
CCGGGTGGGC	ACTTTGCTGC	TTCTTTCTGG	GTTGTGGCCG	ATGAGGCCCT	AAGTAAATAT	1680
GTGAGCATTG	GCCATCAACC	CCATCAAACC	AGCCACAGCC	GTGGAACAGG	CAAGGATGGG	1740
GGCCTGGCCT	GTCCTCTCTG	AATGCCCTTG	AGGGATCCCA	GGAAGCCCCA	GTAGGAGGGA	1800
GCTTCAGACA	GTTCAATTCT	GGCCTGTCTT	CCTTCCCTGC	ACCGGGCAAT	GGGGATAAAG	1860
ATGACTTCGT	AGCAGCACCT	ACTATGCTTC	AGGCATGGTG	CCGGCCTGCC	TCTCC	1915

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Arg	Arg	Ala	Pro	Ser	Leu	Val	Leu	Phe	Phe	Leu	Val	Ala	Leu	Cys
1				5					10					15	
Gly	Arg	Gly	Asn	Cys	Arg	Val	Ala	Asn	Ala	Glu	Glu	Lys	Leu	Met	Asp
			20					25					30		
Asp	Leu	Leu	Asn	Lys	Thr	Arg	Tyr	Asn	Asn	Leu	Ile	Arg	Pro	Ala	Thr
		35					40					45			
Ser	Ser	Ser	Gln	Leu	Ile	Ser	Ile	Lys	Leu	Gln	Leu	Ser	Leu	Ala	Gln
	50					55					60				
Leu	Ile	Ser	Val	Asn	Glu	Arg	Glu	Gln	Ile	Met	Thr	Thr	Asn	Val	Trp
65					70					75					80
Leu	Lys	Gln	Glu	Trp	Thr	Asp	Tyr	Arg	Leu	Thr	Trp	Asn	Ser	Ser	Arg
				85					90					95	
Tyr	Glu	Gly	Val	Asn	Ile	Leu	Arg	Ile	Pro	Ala	Lys	Arg	Ile	Trp	Leu
			100					105					110		
Pro	Asp	Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Thr	Tyr	Glu	Val	Ser
		115					120					125			
Val	Tyr	Thr	Asn	Leu	Ile	Val	Arg	Ser	Asn	Gly	Ser	Val	Leu	Trp	Leu
	130					135					140				
Pro	Pro	Ala	Ile	Tyr	Lys	Ser	Ala	Cys	Lys	Ile	Glu	Val	Lys	Tyr	Phe
145					150					155					160
Pro	Phe	Asp	Gln	Gln	Asn	Cys	Thr	Leu	Lys	Phe	Arg	Ser	Trp	Thr	Tyr
				165					170					175	
Asp	His	Thr	Glu	Ile	Asp	Met	Val	Leu	Met	Thr	Pro	Thr	Ala	Ser	Met
			180					185					190		
Asp	Asp	Phe	Thr	Pro	Ser	Gly	Glu	Trp	Asp	Ile	Val	Ala	Leu	Pro	Gly
		195					200					205			
Arg	Arg	Thr	Val	Asn	Pro	Gln	Asp	Pro	Ser	Tyr	Val	Asp	Val	Thr	Tyr
	210					215					220				
Asp	Phe	Ile	Ile	Lys	Arg	Lys	Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile
225					230					235					240
Ile	Pro	Cys	Val	Leu	Thr	Thr	Leu	Leu	Ala	Ile	Leu	Val	Phe	Tyr	Leu
				245					250					255	
Pro	Ser	Asp	Cys	Gly	Glu	Lys	Met	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu
			260					265					270		
Ala	Leu	Thr	Phe	Phe	Leu	Leu	Leu	Ile	Ser	Lys	Ile	Val	Pro	Pro	Thr

275					280					285					
Ser	Leu	Asp	Val	Pro	Leu	Ile	Gly	Lys	Tyr	Leu	Met	Phe	Thr	Met	Val
290						295				300					
Leu	Val	Thr	Phe	Ser	Ile	Val	Thr	Ser	Val	Cys	Val	Leu	Asn	Val	His
305					310					315					320
His	Arg	Ser	Pro	Ser	Thr	His	Thr	Met	Ala	Pro	Trp	Val	Lys	Arg	Cys
				325					330					335	
Phe	Leu	His	Lys	Leu	Pro	Thr	Phe	Leu	Phe	Met	Lys	Arg	Pro	Gly	Pro
			340					345					350		
Asp	Ser	Ser	Pro	Ala	Arg	Ala	Phe	Pro	Pro	Ser	Lys	Ser	Cys	Val	Thr
			355				360					365			
Lys	Pro	Glu	Ala	Thr	Ala	Thr	Ser	Thr	Ser	Pro	Ser	Asn	Phe	Tyr	Gly
	370					375					380				
Asn	Ser	Met	Tyr	Phe	Val	Asn	Pro	Ala	Ser	Ala	Ala	Ser	Lys	Ser	Pro
385					390					395					400
Ala	Gly	Ser	Thr	Pro	Val	Ala	Ile	Pro	Arg	Asp	Phe	Trp	Leu	Arg	Ser
				405					410					415	
Ser	Gly	Arg	Phe	Arg	Gln	Asp	Val	Gln	Glu	Ala	Leu	Glu	Gly	Val	Ser
			420				425						430		
Phe	Ile	Ala	Gln	His	Met	Lys	Asn	Asp	Asp	Glu	Asp	Gln	Ser	Val	Val
		435					440					445			
Glu	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val	Val	Asp	Arg	Leu	Phe	Leu	Trp
	450					455					460				
Val	Phe	Met	Phe	Val	Cys	Val	Leu	Gly	Thr	Val	Gly	Leu	Phe	Leu	Pro
465					470					475					480
Pro	Leu	Phe	Gln	Thr	His	Ala	Ala	Ser	Glu	Gly	Pro	Tyr	Ala	Ala	Gln
				485					490					495	
Arg	Asp														